## Assessing Multivariate Constraints to Evolution across Ten Long-Term Avian Studies

Celine Teplitsky<sup>1</sup>\*, Maja Tarka<sup>2</sup>, Anders P. Møller<sup>3</sup>, Shinichi Nakagawa<sup>4</sup>, Javier Balbontín<sup>5</sup>, Terry A. Burke<sup>6</sup>, Claire Doutrelant<sup>7</sup>, Arnaud Gregoire<sup>7</sup>, Bengt Hansson<sup>2</sup>, Dennis Hasselquist<sup>2</sup>, Lars Gustafsson<sup>8</sup>, Florentino de Lope<sup>9</sup>, Alfonso Marzal<sup>9</sup>, James A. Mills<sup>10</sup>, Nathaniel T. Wheelwright<sup>11</sup>, John W. Yarrall<sup>12</sup>, Anne Charmantier<sup>7</sup>

1 Département Ecologie et Gestion de la Biodiversité UMR 7204 CNRS/MNHN/UPMC, Muséum National d'Histoire Naturelle, Paris, France, 2 Department of Biology, Lund University, Ecology Building, Lund, Sweden, 3 Laboratoire d'Ecologie, Systématique et Evolution, CNRS UMR 8079, Université Paris-Sud, Orsay, France, 4 Department of Zoology, University of Otago, Dunedin, New Zealand, 5 Department of Zoology, Biology Building, University of Seville, Seville, Spain, 6 Department of Animal and Plant Sciences, University of Sheffield, Sheffield, United Kingdom, 7 Centre d'Ecologie Fonctionnelle et Evolutive UMR 5175 CNRS, Montpellier, France, 8 Department of Animal Ecology, Evolutionary Biology Center, Uppsala University, Uppsala, Sweden, 9 Departamento de Zoología, Universidad de Extremadura, Badajoz, Spain, 10 Corning, New York, United States of America, 11 Department of Biology, Bowdoin College, Brunswick, Maine, United States of America, 12 Lincoln, Christchurch, New Zealand

## Abstract

*Background:* In a rapidly changing world, it is of fundamental importance to understand processes constraining or facilitating adaptation through microevolution. As different traits of an organism covary, genetic correlations are expected to affect evolutionary trajectories. However, only limited empirical data are available.

*Methodology/Principal Findings:* We investigate the extent to which multivariate constraints affect the rate of adaptation, focusing on four morphological traits often shown to harbour large amounts of genetic variance and considered to be subject to limited evolutionary constraints. Our data set includes unique long-term data for seven bird species and a total of 10 populations. We estimate population-specific matrices of genetic correlations and multivariate selection coefficients to predict evolutionary responses to selection. Using Bayesian methods that facilitate the propagation of errors in estimates, we compare (1) the rate of adaptation based on predicted response to selection when including genetic correlations with predictions from models where these genetic correlations were set to zero and (2) the multivariate evolvability in the direction of current selection to the average evolvability in random directions of the phenotypic space. We show that genetic correlations on average decrease the predicted rate of adaptation by 28%. Multivariate evolvability in the direction of current selection and reduced evolvability were due to a general nonalignment of selection and genetic variance, notably orthogonality of directional selection with the size axis along which most (60%) of the genetic variance is found.

*Conclusions:* These results suggest that genetic correlations can impose significant constraints on the evolution of avian morphology in wild populations. This could have important impacts on evolutionary dynamics and hence population persistence in the face of rapid environmental change.

Estimation of the additive genetic (co)variance matrix  ${\bf G}$ 

 $\mathbf{y} = \mu + \mathbf{y} + \mathbf{Z} + \mathbf{Z$ 

Estimating selection

β

able 4. Estimates of mean standardize iterval.	BIL	öd	Wing 0.018	Tarsus 0.041	Mass 0.075	Bill 0.045	Wing:Tarsus 0.01	Wing:Mass 0.012	Wing:Bill 0.008	Tarsus:Mass 0.021		Mass:Bill 0.032	I <sub>A</sub> -evolvabilities were higher for mass than for othe doi:10.1371/journal.pone.0090444.t004			
of mean stand	Blue tit - Muro	posterior mode	18	41	175	45	2	12	08	21	19	32	ner for mass than 0090444.t004			
_		Lowel 9	0.013	0.027	0.042	0.028	0.003	0.002	-0.00	0.006	0.006	0.008				
traits		95%CI											characte			
stimated V <sub>A</sub> ×100	Blue	poste	0.013	0.043	0.079	0.028	0.012	0.012	0.007	0.029	0.013	0.017	c scale of this measu			
V <sub>A</sub> ×100	Blue tit - Pirie	posterior mo											his measu			
		Upper 95%CI	0.018	0.058	0.11	0.041	0.017	0.022	0.011	0.046	0.022	0.03	iaracters were measured on a linear scale [40].			
Ţ	Blue		0.02	0.043	0.103	0.05	0.007	0.017	0.006		0.01		ured on a linea			
ee Blue tit po	Blue tit - Rouvière	posterior mode		~	~				.0				r scale [40].			
ee Blue tit populations with the		Lower 95%CI	0.015	0.035	0.077	0.038	0.002	0.009	0	0.012	0.002	0.015			1	
with		%CI														

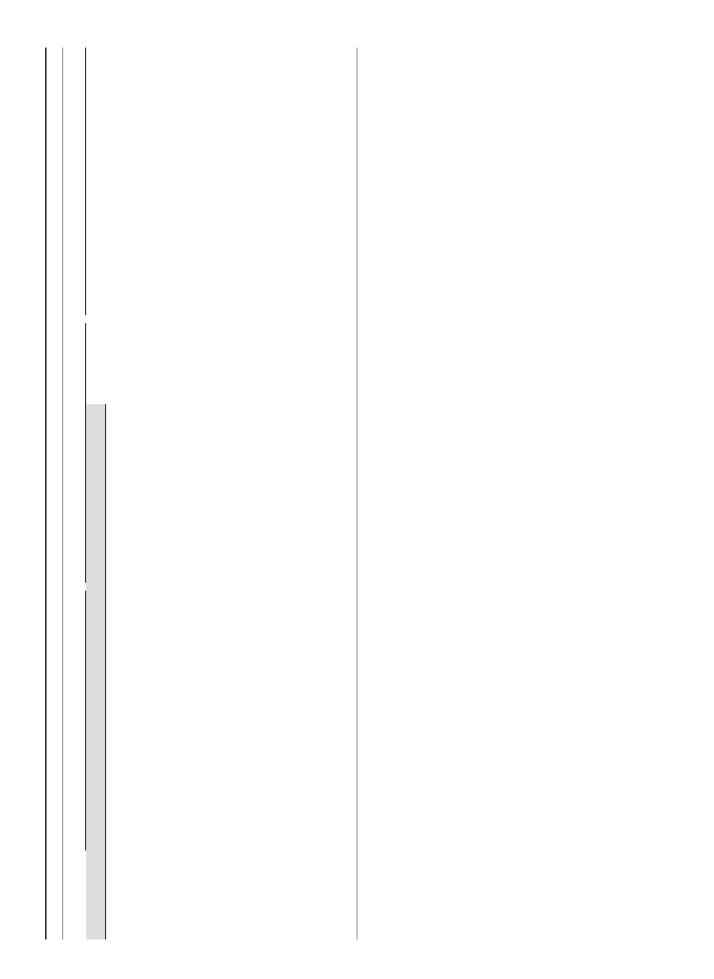
heir 95% confidence

Upper 95%CI 0.054 0.065 0.011 0.024 0.025 0.011 0.131 0.018 0.035 0.042

$$_{\beta} = \frac{\boldsymbol{\beta}^{T} \mathbf{G} \boldsymbol{\beta}}{\left\| \boldsymbol{\beta} \right\|^{2}} \tag{4}$$

Table 7. Estimates of directional and noi intervals.	Table 7. Estimates of directional and non-linear selection gradients for the Red-billed gull, Great reed warbler, an intervals.	d gull, Great reed warbler, ar
Red-billed gull	Great reed warbler	Barn swallow - Bad

	Red-billed gull			Great reed warbler	er		Barn swallow - Bad
	posterior mode Low 95%CI Up 95%CI	Low 95%CI	Up 95%CI	posterior mode Low 95%CI Up 95%CI	Low 95%CI	Up 95%CI	posterior mode
ß	4.22	1.94	7.24	5.23	2.53	8.17	0.54
Wing	1.14	-2.75	5.9	-0.09	-3.79	4.12	0.33
Tarsus	1.86	-1.12	4.39	4.04	1.45	7.69	0.12
Mass	-1.15	-2.39	0.32	-1.78	-3.02	-0.51	0.08
Bill	1.86	-1.83	5.35	0.58	-1.48	1.96	0.15
Wing <sup>2</sup>	139.96	-27.15	243.35	15.61	-107.1	233.37	-13.47
Tarsus <sup>2</sup>	29.1	-33.29	88.21	24.88	-61.64	128.76	2.78
Mass <sup>2</sup>	9.26	27895	2:423:355(35)-7	7			





Natural selection on morphology

## \* \*

## Discussion

۲ • ۲. ۲. ۲ ۲. ا ١ G L ١ ۱. ۱ ١ **\** 

• • • • ١ β

